

Score: 1544.00 Matches: 299
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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Db 16 ATGGGACAAAGGCGCAAGTCGAGAGAACTGTTGTGCTCTTATATGGCGATCTG 75
Qy 21 LeuCysSerLeuAlaLeuGlySerValThrValHisSerSerGluProGluValArg 40
Db 76 TTGTGCTCCCTGGCAATGGCGAGTGTACAGTGCCTCTTCTGAACCTCAAGTCA 135
Qy 41 ProGluAsnProValLysLeuSerCysAlaLysSerGlyPheSerSerProArgVal 60
Db 136 CTGAGATATCTCTGAGTTGCTGCTGCTACTCGGCTTTCTCTCCCGTGTG 195
Qy 61 GluTyrLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr 80
Db 196 GAGTGAAGATTGACCAAGGAGACACCAAGACTGTTGCTATATAACAGATCA 255
Qy 81 AlaSerTyrGluAspArgValThrPheLeuProThrGlyIleThrPheLysSerValThr 100
Db 256 GCTTCCTATGAGACCGGCGTACCTCTTGTGCAACTGCTATCACCTCAAGTCCG 315
Qy 101 ArgGluAspThrGlyThrTyrCysMetValSerGluGluGlyGlyAsnSerTyrGly 120
Db 316 CGGGAAGACACTGGGACATACACTTGTATGGTCTCTGAGGAAGCGCGCAACG 375
Qy 121 GluValLysValLysLeuValLeuValProProSerLysProThrValAsnIlePro 140
Db 376 GAGTCAAGTCAAGTCACTCATCTGCTGTTGCTCTCCATCCAGCTCAGATTAC 435
Qy 141 SerSerAlaThrIleGlyAsnArgAlaValLeuThrCysSerSerGluAspGlySerPro 160
Db 436 TCCTCTGCGCACCATTTGGGAACCGGCGAGTGTGATGCTCAGAACAGATGTTCC 495
Qy 161 ProSerGluTyrThrTyrPheLysAspGlyIleValMetProThrAsnProLysSerThr 180
Db 496 CCTTCTGAATACACTGCTTCAAGATGGGATAGTATGCTTACGAATCCCAAG 555
Qy 181 ArgAlaPheSerAsnSerSerTyrValLeuAsnProThrThrGlyLeuLeuValPheAsp 200
Db 556 CTGCTTCAAGCACTCTCTATGCTGTAATCCCAACAGGAGAGCTGCTCTTTG 615
Qy 201 ProLeuSerAlaSerAspThrGlyLysThrCysGluAlaArgAsnGlyTyrGlyThr 220
Db 616 CCCCTGTGAGCTCTGATCTGAGATACAGTGTGAGGACCGAATGGGTATGG 675
Qy 221 ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsnValGlyValIleVal 240
Db 676 CCCATGACTTCAATGCTGTGCGCATGGAAGCTGTGAGCGCAATGCGGCGTCA 735
Qy 241 AlaAlaValLeuValThrIleLeuLeuGlyIleLeuValPheGlyIleThrPheAla 260
Db 736 GCAGCCGCTCTGTAACTGATCTCTCGGGAATCTTGGTTTGGGATCTCGGTT 795
Qy 261 TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysLysValIleTyr 280
Db 796 TATAGCGAGGCCATTGTGACGACCAAGAAAGAGGACTTTCAGTAAAGGTGATT 855
Qy 281 SerGlnProSerAlaArgSerGluGlyGluPheLysGlnThrSerSerPheLeuVal 299
Db 856 AGCCAGCTAGTGGCCGAGTGAAGAGAAATTCACACAGACCTCTGTCATCTCG 912
RESULT 5
AF207907 1822 bp mRNA linear PRI 14-FEB-2001
LOCUS Homo sapiens platelet FII receptor mRNA, complete cds.
DEFINITION
ACCESSION AF207907

AF207907.1 GI:6653648
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 100 to 175)
AUTHORS Naik, U.P., Ehrlich, Y.H. and Kornecki, E.
TITLE Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a novel platelet receptor for monoclonal antibody FII with the Fc gamma RII receptor
JOURNAL Biochem. J. 310 (Pt 1), 155-162 (1995)
MEDLINE 95374438
PUBMED 7646439
REFERENCE 2 (bases 1 to 1822)
AUTHORS Sobocka, M.B., Sobocki, T., Banerjee, P., Weiss, C., Rushbrook, J.I., Norin, A.J., Hartwig, J., Salifu, M.O., Markell, M.S., Babinska, A., Ehrlich, Y.H. and Kornecki, E.
TITLE Cloning of the human platelet FII receptor: a cell adhesion molecule member of the immunoglobulin superfamily involved in platelet aggregation
JOURNAL Blood 95 (8), 2600-2609 (2000)
MEDLINE 20218744
PUBMED 10753840
REFERENCE 3 (bases 1 to 1822)
AUTHORS Sobocka, M.B., Sobocki, T., Rushbrook, J.I., Banerjee, P., Weiss, C. and Kornecki, E.
TITLE Direct Submission
JOURNAL Submitted (19-NOV-1999) Anatomy and Cell Biology, SUNY, Health Science Center at Brooklyn, 450 Clarkson Ave., Brooklyn, NY 11203, USA
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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16..915
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CDS
Alignment Scores:
Pred. No.: 2,1e-127 Length: 1822
Score: 1544.00 Matches: 299
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-785-220-1 (1-299) x AF207907 (1-1822)
Qy 1 MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPheLeuLeuAlaLeu 20
Db 16 ATGGGACAAAGGCGCAAGTCGAGAGAACTGTTGTGCTCTTATATGGCGATCTG 75
Qy 21 LeuCysSerLeuAlaLeuGlySerValThrValHisSerSerGluProGluValArg 40
Db 76 TTGTGCTCCCTGGCAATGGCGAGTGTACAGTGCCTCTTCTGAACCTCAAGTCA 135
Qy 41 ProGluAsnProValLysLeuSerCysAlaLysSerGlyPheSerSerProArgVal 60

Db 136 CCTGAGATATCTGTGAACTTGTCTGTGCTACTCGGCTTTCTTCTCCCGGTG 195

Qy 61 GluTrpLysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr 80

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Qy 101 ArgGluAspThrGlyThrTyrThrCysMetValSerGluGluGlyGlyAsnSerTyrGly 120

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Qy 181 ArgAlaPheSerAsnSerSerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp 200

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Qy 201 ProLeuSerAlaSerAspThrGlyGluTyrSerCysGluAlaArgAsnGlyTyrGlyThr 220

Db 616 CCCCTGTGCGCTCTGATCTGAGAAATACAGCTGTGAGGACCGAATGGTATGGGACA 675

Qy 221 ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsnValGlyValIleVal 240

Db 676 CCCATGACTTCAATGCTGCGCATGGAAGCTGGAGCGAATGGGGGTTCATCGT 735

Qy 241 AlaAlaValLeuValThrLeuIleLeuLeuGlyIleLeuValPheGlyIleThrPheAla 260

Db 736 GCAGCCGTCTTGTAACTGATCTCTCTGGATCTTGTGTTTGGCATCTGTTGCC 795

Qy 261 TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysLysValIleTyr 280

Db 796 TATAGCCGAGGCCACTTTTGACAGAACAAAGAGGACCTTCGATGAAGAGGTGATTTAC 855

Qy 281 SerGlnProSerAlaArgSerGluGlyGluPheLysGlnThrSerSerPheLeuVal 299

Db 856 AGCCAGCTAGTGCCTGAGGAGGAGATTCAAACAGACCTCGTCAATCTCCGTG 912

RESULT 7

BD175316

LOCUS BD175316 1842 bp DNA linear PAT 18-MAR-2003

DEFINITION Secretory and transmembrane polypeptide and nucleic acid encoding the same.

ACCESSION BD175316

VERSION BD175316.1 GI:29121012

KEYWORDS JP 2002253280-A/98.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.

TITLE Secretory and transmembrane polypeptide and nucleic acid encoding the same

JOURNAL Patent: JP 2002253280-A 98 10-SEP-2002; GENENTECH INC

COMMENT OS Homo sapiens (human)

PN JP 2002253280-A/98

PD 10-SEP-2002

PF 18-DEC-2001 JP 2001385319

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR

18-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR

17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR

21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR

24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR

24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR

24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR

27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063449,28-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR

28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR

28-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR

29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR

29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR

29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR

31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR

07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR

17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR

21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR

24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P7/06, PC

A61P25/00,

PC A61P25/16,A61P25/28,A61P31/12,A61P35/00,C07K14/47,C07K16/18,

PC C07K19/00,

PC C12N1/19,C12N1/21,C12N5/10//A61K38/00,A61K39/395,A61K39/395,

PC A61P43/00,

PC C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),(C12N5/10,

PC C12R1:91),

PC C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12R1:91) CC

Secretory and transmembrane polypeptide and nucleic acid CC

encoding the same

PH Key Location/Qualifiers

FT source 1..1842

FT /organism="Homo sapiens (human)"

FEATURES

source 1..1842

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Alignment Scores:

Pred. No.: 2,13e-127 Length: 1842

Score: 1544.00 Matches: 299

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-785-220-1 (1-299) x BD175316 (1-1842)

Qy 1 MetGlyThrLysAlaGlnValGluArgLysLeuLeuCysLeuPheIleLeuAlaIleLeu 20

Db 52 ATGGGACAAAGCGGCAAGTCGAGAGAACTGTTGGCTCTTCATATGGCGATCTG 111

Qy 21 LeuCysSerLeuAlaLeuGlySerValThrValHisSerSerGluProGluValArgIle 40

Db 112 TTGTGCTCCCTGGCAATGGGCACTGTACAGTGCACCTTCTGAACCTGAAGTCAGAATT 171

Qy 41 ProGluAsnProValLysLeuSerCysAlaTyrSerGlyPheSerSerProArgVal 60

Db 172 CCTGAGAAATATCCTGTGAAGTGTCTGCTGCTACTCGGCTTTCTTCTCCCGGTG 231

Qy 61 GluTriPlysPheAspGlnGlyAspThrThrArgLeuValCysTyrAsnAsnLysIleThr 80

Fax: +49 30 32639 111
www.rzpd.de

This clone is available from RZPD;
contact RZPD (customer.service@rzpd.de) for further information.
This CDS clone is a part of a collection of human full ORF clones
generated by RZPD.

This CDS has been cloned incl. stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att. AAAAAA GCA GGC (ATG).
After the stop codon 3' UTR sequence is present in front of the 3'
att site (ACCCAGCTTTCTT).

Compared to the reference sequence NM_144501 (gi21464106) we did
not find any amino acid exchanges.

Clone distribution: <http://www.rzpd.de/products/orfclones/>.

FEATURES

source

Location/Qualifiers

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gene

CDS

ORIGIN

Alignment Scores:

Pred. No.: 1..11e-127 Length: 1077
Score: 1544.00 Matches: 299
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-785-220-1 (1-299) x CR533512 (1-1077)

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Db 1 ATGGGACAAAGGCGCAAGTCGAGAGAACTGTGTGCTCTTCATATTGGCGATCTG 60
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Qy 41 ProGluAsnAsnProValLysLeuSerCysAlaTyrSerGlyPheSerProArgVal 60
Db 121 CCTGAGATATCTCTGTGAAGTGTCTGTGCTACTCGGCTCTTCTTCTCCCGGTG 180
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Db 241 GCTTCTATGAGGACCGGGTACCTCTTCTGCAACTGTGTATCATCTTCAAGTCGTCACA 300
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Db 301 CGGNAGACACTGGGACATACACTTGATGTGCTCTGAGGAAGCGGCAACAGCTATGGG 360

Qy 121 GluValLysValLysLeuLleValLeuValProProSerLysProThrValAsnLlePro 140
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Qy 141 SerSerAlaThrLleGlyLeuAsnArgAlaValLeuThrCysSerGluGlnAspGlySerPro 160
Db 421 TCCTCTGCCACCAATTGGGAACCGGCGAGTGTGCATGCTCAGAACAGATGGTTCGCCA 480
Qy 161 ProSerGluTyrThrTrpPheLysAspGlyLleValMetProThrAsnProLysSerThr 180
Db 481 CCTTCTGAATACACCTGGTTCAAGATGGGATAGTATGCTACGAAATCCCAAAAGCACC 540
Qy 181 ArgAlaPheSerAsnSerSerTyrValLeuAsnProThrThrGlyGluLeuValPheAsp 200
Db 541 CGTGCCTTTCAGCAACTCTTCTCTATGTCTCTGAATCCCAACAGGAGAGCTGGTCTTTGAT 600
Qy 201 ProLeuSerAlaSerAspThrGlyTyrSerCysGluAlaArgAsnGlyTyrGlyThr 220
Db 601 CCCTGTGACCTCTGTACTGGAGATACAGCTGTGAGGACGGAATGGGTATGGGACA 660
Qy 221 ProMetThrSerAsnAlaValArgMetGluAlaValGluArgAsnValGlyValLleVal 240
Db 661 CCCATGACTTCAAAATGCTGTGCGCATGGAAGCTGTGGAGCGGAATGTGGGGTTCATCGTG 720
Qy 241 AlaAlaValLeuValThrLleLleLeuGlyLleLeuValPheGlyLleTrpPheAla 260
Db 721 GCAGCCGTCCTCTTAACCTGATTCTCTCTGGGAATCTTGTGTCATCTGGTGTGCC 780
Qy 261 TyrSerArgGlyHisPheAspArgThrLysLysGlyThrSerSerLysValLleTyr 280
Db 781 TATAGCGGAGCGGCACCTTTGACAGACAAAGAGGACTTCGAGTAAAGAGGTGATTAC 840
Qy 281 SerGlnProSerAlaArgSerGluGlyGluPheLysGlnThrSerSerPheLeuVal 299
Db 841 AGCCAGCTAGTGCCTGCGAGTGAAGAGATTCAACAGACCTCGTCTATCTCTGCTG 897

RESULT 2

AR201016

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

US-10-785-220-1 (1-299) x AR201016 (1-1140)

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

7/10/1997 (e-date)

Wet cell

+ Vector

